



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Boo

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Display Show:

☐ 1: [NM_173674](#). Homo sapiens disc...[gi:27735142]

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LOCUS NM_173674 2010 bp mRNA linear PRI 05-OCT-2003
 DEFINITION Homo sapiens discoidin, CUB and LCCL domain containing 1 (DCBLD1), mRNA.

ACCESSION NM_173674
 VERSION NM_173674.1 GI:27735142

KEYWORDS .
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2010)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from [BC035671.1](#).

FEATURES Location/Qualifiers

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Spermadhesins contain only this domain"
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The bacterial examples are not yet included in the SEED
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Oct 2 2003 18:31:01

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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vs /tmp/fastaEAAF.aqrX library
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2010 residues in 1 sequences

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Scan time: 0.116

The best scores are:

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99.932% identity in 1464 nt overlap (1-1464:282-1745)

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	40 50 60 70 80 90			
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	160 170 180 190 200 210			
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	440 450 460 470 480 490			
	220 230 240 250 260 270			
LEX	TTGAACACAAGTGAAGTAACCGTCCGCTTTGAGAGTGGATCCCACATTTCTGGCCGGGGT			
			
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	280 290 300 310 320 330			
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          400      410      420      430      440      450
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gi|277   GGAGACATTCTGGGAATATGGTAGATGGATATAGAGATACCTCTTTATTGTGCAAAGCT
          680      690      700      710      720      730

          460      470      480      490      500      510
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gi|277   GCCATCCATGCAGGAATAATTGCTGATGAACTAGGTGGCCAGATCAGTGTGCTTCAGCGC
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          520      530      540      550      560      570
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gi|277   AAAGGGATCAGTCGATATGAAGGGATTCTGGCCAATGGTGTCTTTTCAGGGATGGTTCC
          800      810      820      830      840      850

          580      590      600      610      620      630
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gi|277   CTGTCAGACAAGCGATTCTGTTTACCTCCAATGGTTGCAGCAGATCCTTGAGTTTGA
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          640      650      660      670      680      690
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gi|277   CCTGACGGGCAAATCAGAGCTTCTTCCTCATGGCAGTCGGTCAATGAGAGTGGAGACCA
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          700      710      720      730      740      750
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gi|277   GTTCACTGGTCTCCTGGCCAAGCCCGACTTCAGGACCAAGGCCCATCATGGGCTTCGGGC
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          760      770      780      790      800      810
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gi|277   GACAGTAGCAACAACCAACCAACACGAGAGTGGCTGGAGATCGATTGGGGGAGAAAAAG
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          820      830      840      850      860      870
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          880      890      900      910      920      930
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gi|277   AGTTTTGTGATGAACCTCAAAAACAATAATCTAAGTGAAGACCTATAAAGGAATTGTG
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          940      950      960      970      980      990
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          1000      1010      1020      1030      1040      1050
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gi|277   TTCATCCCTCCCATCGTGGCCAGATATGTGCGGGTTGTCCCCCAGACATGGCACCAGAGG
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          1060      1070      1080      1090      1100      1110
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gi|277   ATAGCCTTGAAGGTGGAGCTCATTGGTTGCCAGATTACACAAGGTAATGATTCAATTGGTG
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          1120      1130      1140      1150      1160      1170
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gi|277   TGGCGCAAGACAAGTCAAAGCACCAGTGTTCACCTAAGAAAGAAGATGAGACAATCACA
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      1750      1760      1770      1780      1790      1800

      460      450      440      430      420      410
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      : : : : : : : : : : : : : : : : : :
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1464 residues in 1 query sequences

2010 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon Oct 6 13:26:41 2003 done: Mon Oct 6 13:26:41 2003

Scan time: 0.116 Display time: 0.100

Function used was FASTA